



Version with Markings to Show Changes Made:

In the Specification:

Please revise the first full paragraph on page 1 to read as follows:

This application is a divisional of U.S. Patent Application Serial No. 09/330,970 filed on June 11, 1999, now U.S. Patent No. 6,146,876 [which was filed as a continuation-in-part of U.S. Patent Application Serial No. 09/277,423 filed on March 26, 1999].

Please revise the paragraph beginning at the bottom of page 7 to read as follows:

Figure 2 shows a comparison of the long phosphodiesterase against the Prosite database of protein patterns, specifically showing a high score against the 3' 5' cyclic nucleotide phosphodiesterase Family 7 (SEQ ID NO:5). The underlined area shows a phosphodiesterase signature.

Please revise the second full paragraph on page 8 to read as follows:

Figure 4 shows a hydrophobicity plot of the long phosphodiesterase (SEQ ID NO:1).

Please revise the third full paragraph beginning on page 8 to read as follows:

Figure 5 shows an analysis of the long phosphodiesterase open reading frame (SEQ ID NO:1) for amino acids corresponding to specific functional sites. Glycosylation sites are found from about amino acid 107 to about amino acid 110, from about amino acid 290 to about amino acid 293, and from about amino acid 447 to about amino acid 450. A glycosaminoglycan attachment site is found from about amino acid 479 to about amino acid 482. Cyclic AMP and cyclic GMP-dependent protein kinase phosphorylation sites are found from about amino acid 15 to about amino acid 18 and from about amino acid 94 to about amino acid 97. Protein kinase C phosphorylation sites are found from about amino acid 117 to about amino acid 119 and from about amino acid 390 to about amino acid 392. Casein kinase II phosphorylation sites are found from about amino acid 18 to about amino acid 21, from about amino acid 56 to about amino acid 59,



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from about amino acid 251 to about amino acid 254, from about amino acid 292 to about amino acid 295, from about amino acid 449 to about amino acid 452, from about amino acid 481 to about amino acid 484, and from about amino acid 492 to about amino acid 495. A tyrosine kinase phosphorylation site is found from about amino acid 392 to about amino acid 398. N-myristoylation sites are found from about amino acid 22 to about amino acid 27, from about amino acid 29 to about amino acid 34, from about amino acid 67 to about amino acid 72, from about amino acid 258 to about amino acid 263, and from about amino acid 477 to about amino acid 482. An amidation site is found from about amino acid 13 to about amino acid 16. In addition, amino acids corresponding to the phosphodiesterase signature, HDXXHXX, are found in the sequence HDVDHPG at amino acids 265-271.

Please revise the second full paragraph on page 9 to read as follows:

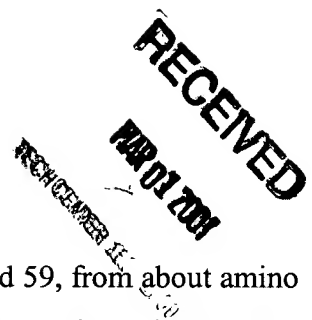
Figure 7 shows a comparison of the short phosphodiesterase against the Prosite database of protein patterns, specifically showing a high score against the 3' 5' cyclic nucleotide phosphodiesterase Family 7 (SEQ ID NO:6). The underlined area shows a phosphodiesterase signature.

Please revise the third full paragraph on page 9 to read as follows:

Figure 8 shows a hydrophobicity plot of the short phosphodiesterase (SEQ ID NO:3).

Please revise the last full paragraph on page 9 to read as follows:

Figure 9 shows an analysis of the short phosphodiesterase open reading frame SEQ ID NO:3) for amino acids corresponding to specific functional sites. Glycosylation sites are found from about amino acid 107 to about amino acid 110 and from about amino acid 290 to about amino acid 293. Cyclic AMP and cyclic GMP-dependent protein kinase phosphorylation sites are found from about amino acid 15 to about amino acid 18 and from about amino acid 94 to about amino acid 97. Protein kinase C phosphorylation sites are found from about amino acid 117 to about amino acid 119. Casein kinase II phosphorylation sites are found from about amino



acid 18 to about amino acid 21, from about amino 56 to about amino acid 59, from about amino acid 251 to about amino acid 254, and from about amino acid 292 to about amino acid 295. N-myristoylation sites are found from about amino acid 22 to about amino acid 27, from about amino acid 29 to about amino acid 34, from about amino acid 67 to about amino acid 72, from about amino acid 258 to about amino acid 263, and an amidation site is found from about amino acid 13 to about amino acid 16. In addition, amino acids corresponding to the phosphodiesterase signature, HDXXHXX, are found in the sequence HDVDHPG at amino acids 265-271.